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Rediscovery and revalidation of *Sinomicrurus wongii* Fan, 1931 (Squamata, Elapidae), from South China and northern Vietnam following nearly a century of obscurity

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Abstract

At present, both *Calliophis wongii* Fan, 1931, and *Sinomicrurus houi* Wang, Peng & Huang, 2018, are regarded as junior synonyms of *Sinomicrurus kelloggi*. In this study, we revalidate the species status of *C. wongii* based on morphological and molecular evidence and confirm *S. houi* as a junior synonym of *C. wongii*. Two road-killed specimens of *Sinomicrurus* were collected from Napo in 2024, which morphologically best match the original description of *C. wongii*. Analyses of the mitochondrial COI and Cyt *b* genes reveal that these specimens form a well-supported clade with *S. houi* (uncorrected *p*-distance: 1.3% for COI, <2% for Cyt *b*) but are significantly divergent from *S. kelloggi* (7.7% for COI, 5.5–6.1% for Cyt *b*), values that exceed the commonly accepted interspecific threshold within the genus. *Sinomicrurus wongii* **comb. nov.** is mainly distinguished from *S. kelloggi* by possessing seven infralabials and narrow black dorsal bands. Based on available data, we also clarify the distribution of *C. wongii*, which occurs in Guangxi, Yunnan, and Hainan, China, as well as in Hai Duong and Cao Bang, Vietnam.

Key Words

Morphology, *Sinomicrurus houi*, *Sinomicrurus kelloggi*, *Sinomicrurus wongii* comb. nov., systematics, taxonomy

Introduction

The genus *Sinomicrurus* is a genus of small- to medium-sized venomous snakes belonging to the family Elapidae. It was formally established by Slowinski et al. (2001) based on morphological and molecular systematic evidence. Currently, the genus *Sinomicrurus* comprises 10 species, namely *S. annularis* (Günther, 1864), *S. boettgeri* (Fritze, 1894), *S. gorei* (Wall, 1909), *S. iwasakii* (Maki, 1935), *S. japonicus* (Günther, 1868), *S. kelloggi* (Pope, 1928), *S. macclellandi* (Reinhardt, 1844), *S. peinani* Liu, Yan, Hou, Wang, Nguyen, Murphy, Che & Guo, 2020, *S. sauteri* (Steindachner, 1913), and *S. swinhoei* (Van Denburgh, 1912) (Smart et al. 2021; Uetz et al. 2026).

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Pope (1928) formally described *Hemibungarus kelloggi* based on four specimens collected from Ch'ungan County (now part of Wuyishan City), Fujian Province, China. This species was later assigned to *Sinomicrurus*. It is characterized by 15 midbody dorsal scale rows, no trunk longitudinal stripes, and a distinct head–neck separation. Fan (1931) described *Calliophis wongii* based on two specimens from Loshiang (now Luoxiang Township, Jinxiu Yao Autonomous County, Guangxi, China), which also possesses 15 dorsal scale rows. Morphologically, *C. wongii* differs from *H. kelloggi* by a shorter tail and narrower white head bands. Bourret (1935) later described the subspecies *C. wongii tonkinensis* from Vietnam. Peng et al. (2018) described *S. houi* as a new species from Hainan Island, China. However, Smart et al. (2021) synonymized it with *S. kelloggi*, citing overlapping morphological variation and a lack of resolved phylogenetic monophyly, and argued that inconsistencies in prior mitochondrial topologies were likely due to sequence misalignment or sample misidentification (Smart et al. 2021).

In June 2024, two coral snake specimens were collected from Napo County, Baise City, Guangxi Zhuang Autonomous Region, China. Morphologically, these specimens match the original description of *Calliophis wongii* Fan, 1931. They possess 15 dorsal scale rows and dorsal black transverse bands that are half a scale in width. The presence of two white transverse bands on the head and the relatively short tail length in males closely correspond to the holotype of *C. wongii*. This half-scale band width is consistent with that reported for *S. houi* (Peng et al. 2018), yet distinct from the one-scale-wide bands characteristic of *S. kelloggi* (Fig. 1). Phylogenetically, the Napo specimens cluster with *S. houi* to form a sister clade to *S. kelloggi*. The uncorrected *p*-distance between Napo specimens and *S. houi* is only 1.3% based on COI, whereas it reaches 7.7% with *S. kelloggi*. This divergence exceeds the known interspecific distances within the genus (e.g., *S. annularis* and *S. swinhoei*). Consistent results were obtained for the Cyt *b* gene. Therefore, integrating morphological and molecular evidence, we identify the two Napo specimens as *C. wongii*, restore its status as an independent species, synonymize *S. houi* with *C. wongii*, and reassign the latter to the genus *Sinomicrurus* as *Sinomicrurus wongii* comb. nov.

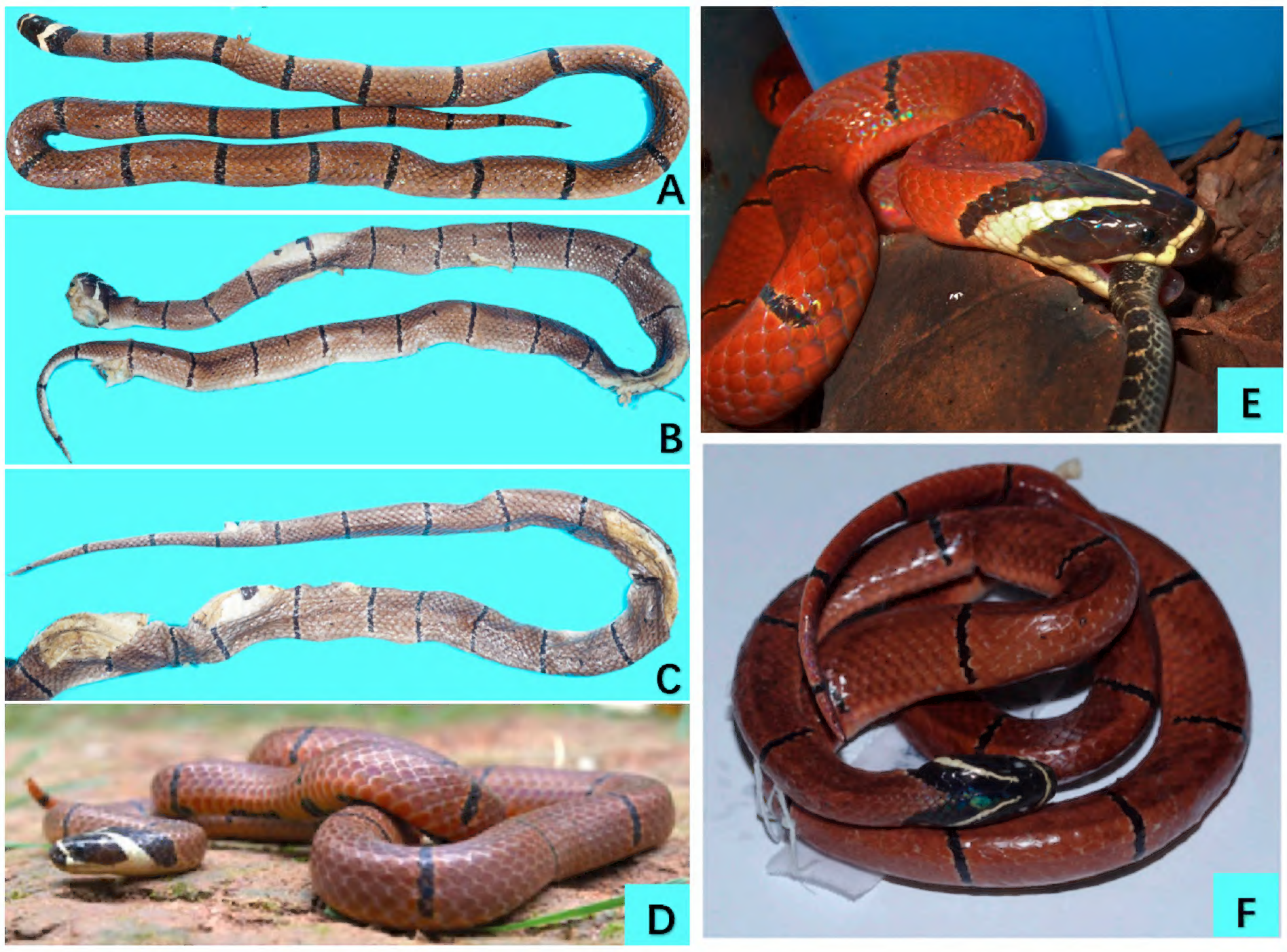

Figure 1. Comparison of dorsal black transverse band width between *S. wongii* comb. nov. and *S. kelloggi*: **A.** *S. kelloggi* (GXNU2025110601) from Liuzhou, Guangxi; **B, C.** *S. wongii* comb. nov. (GXNU2024061701, GXNU2024061702) from Napo, Baise, Guangxi; **D.** *S. wongii* comb. nov. from Yunnan (Sun et al. 2015); **E, F.** *S. wongii* comb. nov. from Hainan (Peng et al. 2018). The black rings on *S. kelloggi* are approximately one scale in width, whereas those on *S. wongii* comb. nov. are only 0.5 scale in width.

Materials and methods

Sampling

In June 2024, two road-killed specimens (vouchers: GXNU2024061701 and GXNU2024061702) of the genus *Sinomicrurus* were collected from Napo County, Baise, Guangxi Zhuang Autonomous Region, China (Fig. 2). Our researchers additionally collected one *Sinomicrurus* individual (voucher: GXNU2025110601) from Rongshui Miao Autonomous County, Liuzhou, Guangxi Zhuang Autonomous Region. All specimens were fixed and preserved in 80% ethanol and are currently deposited in the Museum of the School of Life Sciences, Guangxi Normal University.

Molecular phylogenetic analysis

Genomic DNA was extracted from the muscle tissue of the collected specimens using the TIANamp Marine Animals DNA Kit (TIANGEN Biotech). The COI gene was amplified with primers Chmf4/Chmr4 (Che et al. 2012), and the Cyt *b* gene with primers H16064-R (5′-CTTTGGTTTACAAGAACAATGCTTTA-3′) and Gludg-F (5′-AACCACCGTTGTACATCAACT-3′). PCR amplification was performed in 25 μL reactions containing 12.5 μL 2× SanTaq PCR Master Mix (with Blue Dye), 10 μL ddH_2O, 1 μL F-primer, 1 μL R-primer, and 0.5 μL DNA template. The PCR conditions were an initial denaturing step at 94 °C for 5 min, followed by 35 cycles: denaturing at 94 °C for 30 s, annealing at 48.5 °C for 45 s, an extension step at 72 °C for 35 s, and a final extension at 72 °C for 10 min. Finally, the PCR products were sent to Sangon Biotechnologies Co., Ltd. (Shanghai, China), where the purified PCR products were sequenced using the same forward and reverse primers.

Sequencing peak maps were manually corrected. We downloaded 39 COI and 37 Cyt *b* sequences of *Sinomicrurus* from GenBank (Tables 1, 2). For the phylogenetic analysis based on the COI gene, *Micrurus nigrocinctus* and *Micrurus lemniscatus* were selected as outgroups (Liu et al. 2020), whereas *Hemibungarus calligaster* and *Micrurus fulvius* were designated as outgroups for the phylogenetic analysis based on the Cyt *b* gene (Smart et al. 2021). All sequences were aligned with the retrieved sequences of the same gene locus using MEGA X software (Kumar et al. 2018). PartitionFinder 2 software was used to select the most suitable nucleotide substitution models separately for the Cyt *b* and COI sequence datasets, based on the Akaike Information Criterion (AIC) (Lanfear et al. 2017). After that, separate phylogenetic trees were constructed based on the COI and Cyt *b* genes using PhyloSuite 1.2.3 (Zhang et al. 2020). For the COI gene dataset, the Maximum Likelihood (ML) tree was constructed with IQ-TREE (Nguyen et al. 2015) under the best-fit GTR+G model using 1000 standard bootstrap approximations, and the Bayesian Inference (BI) tree was built with MrBayes 3.2.7 (Ronquist et al. 2012) under the same best-fit GTR+G model, running for 2,000,000 generations with the initial 25% of the sampled data discarded as burn-in. For the Cyt *b* gene dataset, the ML tree and BI tree were constructed using the same software and parameters but under the best-fit GTR+I+G model.

Morphological analysis

Thirteen meristic characters were recorded: bands on body (Bands), bands on tail (Tail Bands), the numbers of dorsal scale rows (DSR, counted at one head length behind the head, at midbody, and at one head length before the vent), infralabials (IL), loreal (Lor) at left and right, postoculars (PostOc), preoculars (PreOc), subcaudal plates (SC, the terminal scute excluded from the number of subcaudals), supralabials (SL), temporals (Tem), ventral plates (VEN), and the number of blotches and spots on the ventral and subcaudal parts. Three morphometric characters were measured: snout–vent length (SVL), tail length (TaL), and total length (TL).

Body and tail lengths were measured using a ruler to the closest 1 mm. Terminology for scale counts follows standard colubrid terminology (e.g., Smith and Campbell 1994; Smith et al. 2008; Vogel and David 2010; Vogel and Luo 2011).

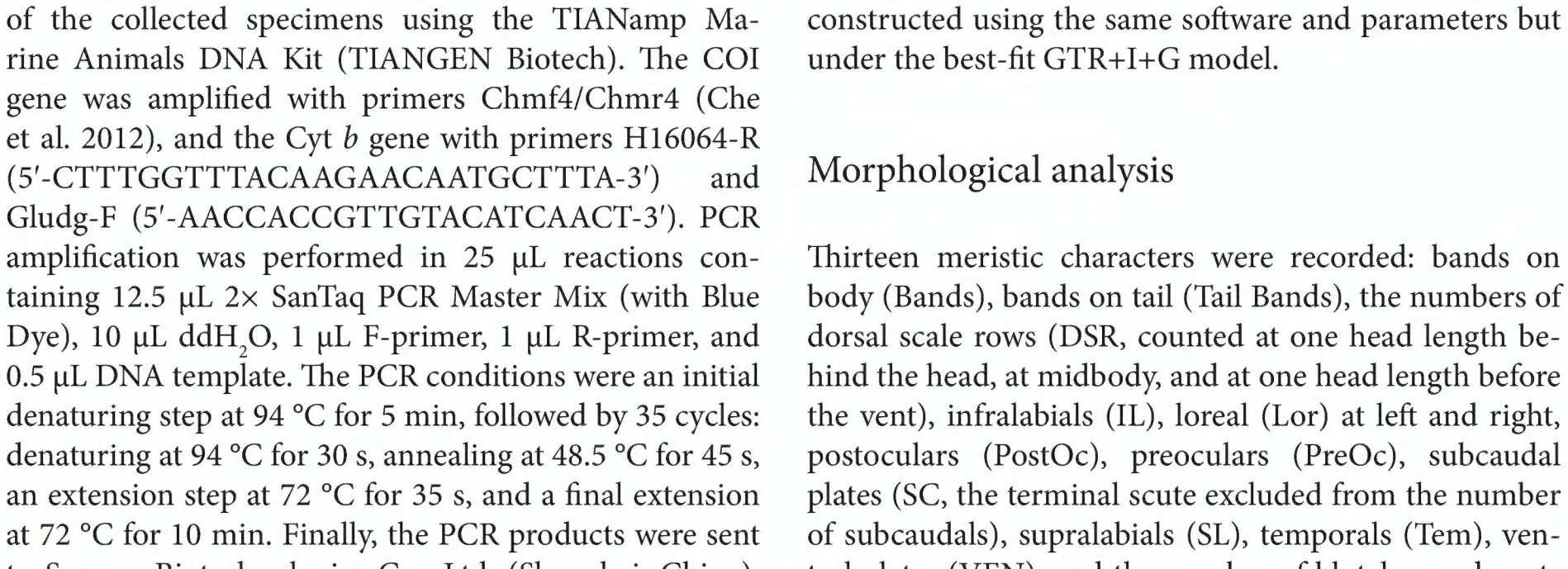

Figure 2. The two road-killed specimens of *S. wongii* comb. nov. from Napo, Baise: **A.** GXNU2024061701; **B.** GXNU2024061702.

Table 1. Samples used for molecular phylogenetic analysis of the COI gene in this study.

No.	Taxa	Voucher	Locality	COI
1	*S. wongii* comb. nov. (This study)	GXNU2024061701	Baise, China	—
2	*S. wongii* comb. nov. (This study)	GXNU2024061702	Baise, China	—
3	*S. kelloggi* (This study)	GXNU2025110601	Liuzhou, China	—
4	*S. sauteri*	RN 0285	Taiwan, China	KP749804
5	*S. sauteri*	RN 0726	Taiwan, China	KP749810
6	*S. sauteri*	RN 0745	Taiwan, China	KP749812
7	*S. sauteri*	RN 1581	Taiwan, China	KP749827
8	*S. sauteri*	RN 1455	Taiwan, China	KP772310
9	*S. peinani*	YBU 16054	Guangxi, China	MN685879
10	*S. peinani*	YBU 16086	Guangxi, China	MN685882
11	*S. peinani*	YBU 16067	Guangxi, China	MN685881
12	*S. peinani*	YPX 9245	Cao Bang, Vietnam	MN685894
13	*S. peinani*	YBU 16066	Guangxi, China	MN685880
14	*S. peinani*	YPX 9247	Vinh Phuc, Vietnam	MN685896
15	*S. peinani*	YPX 9246	Vinh Phuc, Vietnam	MN685895
16	*S. peinani*	YPX 9244	Cao Bang, Vietnam	MN685893
17	*S. annularis*	KIZ 011981	China	MN685886
18	*S. annularis*	ROM 37110	Vietnam	MN685891
19	*S. annularis*	YPX 9241	Vietnam	MN685890
20	*S. annularis*	GP 2742	Fujian, China	MN685877
21	*S. annularis*	GP 3360	Sichuan, China	MN685878
22	*S. annularis*	GP 5500	Sichuan, China	MN685885
23	*S. annularis*	GP1059	Hainan, China	MN685873
24	*S. swinhoei*	RN 0611	Taiwan, China	KP749807
25	*S. swinhoei*	RN 0749	Taiwan, China	KP749813
26	*S. swinhoei*	RN 1024	Taiwan, China	KP749817
27	*S. swinhoei*	RN 0658	Taiwan, China	KP749808
28	*S. kelloggi*	FJHSHS 01	China	MG788980
29	*S. kelloggi*	CHS 031	Nanling, Guangdong, China	MK064599
30	*S. kelloggi*	GP 2194	Guangdong, China	MN685876
31	*S. kelloggi*	CHS 033	Yunnan, China	MK064601
32	*S. kelloggi*	HS 12065	Chenzhou, Hunan, China	OQ416864
33	*S. kelloggi*	HS 12047–2	Chenzhou, Hunan, China	OQ416854
34	*S. kelloggi*	HS 12046	Honghe, Yunnan, China	OQ416861
35	*S. kelloggi*	WYF 00161	Suichang, Zhejiang, China	OQ416875
36	*S. wongii* comb. nov.	CHS 854	Hainan, China	MK064918
37	*S. wongii* comb. nov.	GP 2193	Hainan, China	MN685875
38	*S. wongii* comb. nov.	GP 4643	Hainan, China	MN685883
39	*S. wongii* comb. nov.	ROM 37079	Hai Duong, Vietnam	MN685889
40	*S. wongii* comb. nov.	HS 11224	Jianfengling, Hainan, China	OQ416853
41	*S. wongii* comb. nov.	KIZ 026444	Shangsi, Guangxi, China	OQ416315
42	*S. wongii* comb. nov.	HS 11140	Jianfengling, Hainan, China	OQ416852
43	*Micrurus nigrocinctus*	CH: 5291	Panama	MH140289
44	*Micrurus lemniscatus*	USNM: Herp: 314704	Trinidad and Tobago	MH274442

Result

Morphological results

Morphometric and meristic data of the three collected specimens, alongside the *C. wongii* holotype/paratype; one *Sinomicrurus* discovered in Laojunshan, Yunnan (Sun et al. 2015); and *S. houi* (Peng et al. 2018), are summarized in Table A1.

Molecular results

The COI dataset contains 44 samples with a total of 630 base pairs, and the Cyt *b* dataset includes 42 samples with a total of 1050 base pairs. The phylogenetic topologies resulting from Bayesian inference (BI) and maximum likelihood analysis (ML) are generally consistent in phylogenetic structure (Figs 3, 4).

Phylogenetic analyses based on the COI gene revealed that the two specimens (GXNU2024061701 and GXNU2024061702) from Napo first cluster into a small clade with *S. houi* from Shangsi (KIZ 026444) and *S. houi* from Hai Duong (ROM 37079). Subsequently, this small clade forms a large clade with high support values (100% for BI and 100% for ML) together with the *Sinomicrurus* specimens from Hainan. Among these Hainan specimens are the paratypes of *S. houi* (HS 11140 and HS 11224) and the specimen (CHS 854) identified as *S. kelloggi*. This large clade is more closely related to *S. kelloggi* than to other known species, with strong Bayesian posterior probabilities and high bootstrap support (100% for BI and 96% for ML). The specimen (GXNU2025110601) from Rongshui clusters within the clade of *S. kelloggi*. In contrast, phy-

Table 2. Samples used for molecular phylogenetic analysis of the Cyt *b* gene in this study.

No.	Taxa	Voucher	Locality	Cyt *b*
1	*S. wongii* comb. nov. (This study)	GXNU2024061701	Baise, China	—
2	*S. wongii* comb. nov. (This study)	GXNU2024061702	Baise, China	—
3	*S. kelloggi* (This study)	GXNU2025110601	Liuzhou, China	—
4	*S. annularis*	CIBHN 05	—	MG653602
5	*S. annularis*	CIBHN 06	—	MG653603
6	*S. annularis*	KU 312170	Guizhou, China	MW788934
7	*S. annularis*	ROM 31158	Tuyen Quang, Vietnam	AF217816
8	*S. annularis*	CHS 853	China	MK201569
9	*S. annularis*	CHS 032	China	MK201248
10	*S. boettgeri*	KUZ R-47847	Okinawajima, Japan	LC094046
11	*S. boettgeri*	KUZ R-33165	Okinawajima, Japan	MW788937
12	*S. boettgeri*	KUZ R-72420	Iejima, Japan	LC094045
13	*S. boettgeri*	KUZ R-63292	Tokashikijima, Japan	LC094057
14	*S. boettgeri*	KUZ R-33075	Kumejima, Japan	LC094050
15	*S. iwasakii*	KUZ R-48123	Ishigakijima, Japan	LC094069
16	*S. iwasakii*	KUZ R-48123	Ishigakijima, Japan	MW788939
17	*S. japonicus*	KUZ R-38057	Tokunoshima, Japan	LC094067
18	*S. japonicus*	KUZ R-34576	Tokunoshima, Japan	LC094063
19	*S. japonicus*	KUZ R-33033	Amamioshima, Japan	LC094059
20	*S. japonicus*	KUZ R-33074	Amamioshima, Japan	MW788936
21	*S. japonicus*	KUZ R-72609	Kakeromajima, Japan	LC094075
22	*S. wongii* comb. nov.	ROM 37080	Hai Duong, Vietnam	EF137417
23	*S. wongii* comb. nov.	ROM 35247	Cao Bang, Vietnam	AF220408
24	*S. wongii* comb. nov.	CHS 854	Hainan, China	MK201570
25	*S. kelloggi*	CHS 033	Yunnan, China	MK201249
26	*S. kelloggi*	CHS 031	Nanling, Guangdong, China	MK201247
27	*S. macclellandi*	SH 2872	Nepal	AF220409
28	*S. macclellandi*	MZMU 270	Mizoram State, India	MW788935
29	*S. macclellandi*	BWS OPA-S8	Mongar District, Bhutan	MW788930
30	*S. macclellandi*	CAS 221494	Kachin State, Myanmar	MW788923
31	*S. peinani*	KU 311567	Guangxi, China	MW788932
32	*S. peinani*	KU 311568	Guangxi, China	MW788933
33	*S. peinani*	ROM 35245	Cao Bang, Vietnam	EF137418
34	*S. peinani*	—	—	MZ230594
35	*S. sauteri*	NTNUB NA	Nantou County, Taiwan	MW788929
36	*S. sauteri*	TESRI 2007.10.x	Taitung County, Taiwan	MW788928
37	*S. sauteri*	TESRI 132	Yilan County, Taiwan	MW788926
38	*S. sauteri*	NTNUB 241514	Taoyuan County, Taiwan	MW788924
39	*S. sauteri*	NTNUB 241513	Hsinchu County, Taiwan	MW788925
40	*S. swinhoei*	NMNS 17522	Nantou County, Taiwan	MW788927
41	*Hemibungarus calligaster*	KU 307474	Quezon Island, Philippines	MW788931
42	*Micrurus fulvius*	CAS 214347	Florida State, USA	KU754355

logenetic analyses based on the Cyt *b* gene showed that the two specimens collected from Napo clustered into a clade together with two *Sinomicrurus* specimens from northern Vietnam (ROM 37080 and ROM 35247) and the specimen (CHS 854) from Hainan, China. The specimen (GXNU2025110601) collected from Rongshui grouped into a clade with high support values together with two specimens from Guangdong and Yunnan, China (100% posterior probability for BI and 90% bootstrap support for ML). These two clades further formed a pair of sister clades with extremely high support values (100% posterior probability for BI and 94% bootstrap support for ML).

After removing outgroup taxa, MEGA X was used to calculate uncorrected pairwise sequence divergence between the *Sinomicrurus* species (Tables 3, 4). The genetic distance (uncorrected *p*-distance) between the Rongshui specimen (GXNU2025110601) and *S. kelloggi* is 0.2–0.9% based on the COI gene sequence and 0.0–1.2% based on the Cyt *b* gene sequence. Consequently, this specimen is identified as *S. kelloggi* via morphological and molecular analyses. Phylogenetic analyses based on the COI gene sequences revealed that the minimum uncorrected *p*-distance between the Napo specimens and *S. kelloggi* was 7.7%, whereas the maximum uncorrected *p*-distance between the Napo specimens and *S. wongii* comb. nov. reached 1.3%. The sample (CHS 854) has a genetic divergence ranging 0.0–1.3% between itself and *S. wongii* comb. nov., whereas the genetic distance between this sample and *S. kelloggi* ranges 8.8–9.2%. This pattern is exactly consistent with that observed for the two specimens obtained from Napo. In addition, the uncorrected *p*-distance based on the COI gene between the known species *Sinomicrurus annularis* and *Sinomicrurus swinhoei* ranges 3.3–4.0%. Therefore, we conclude that this *Sinomicrurus*

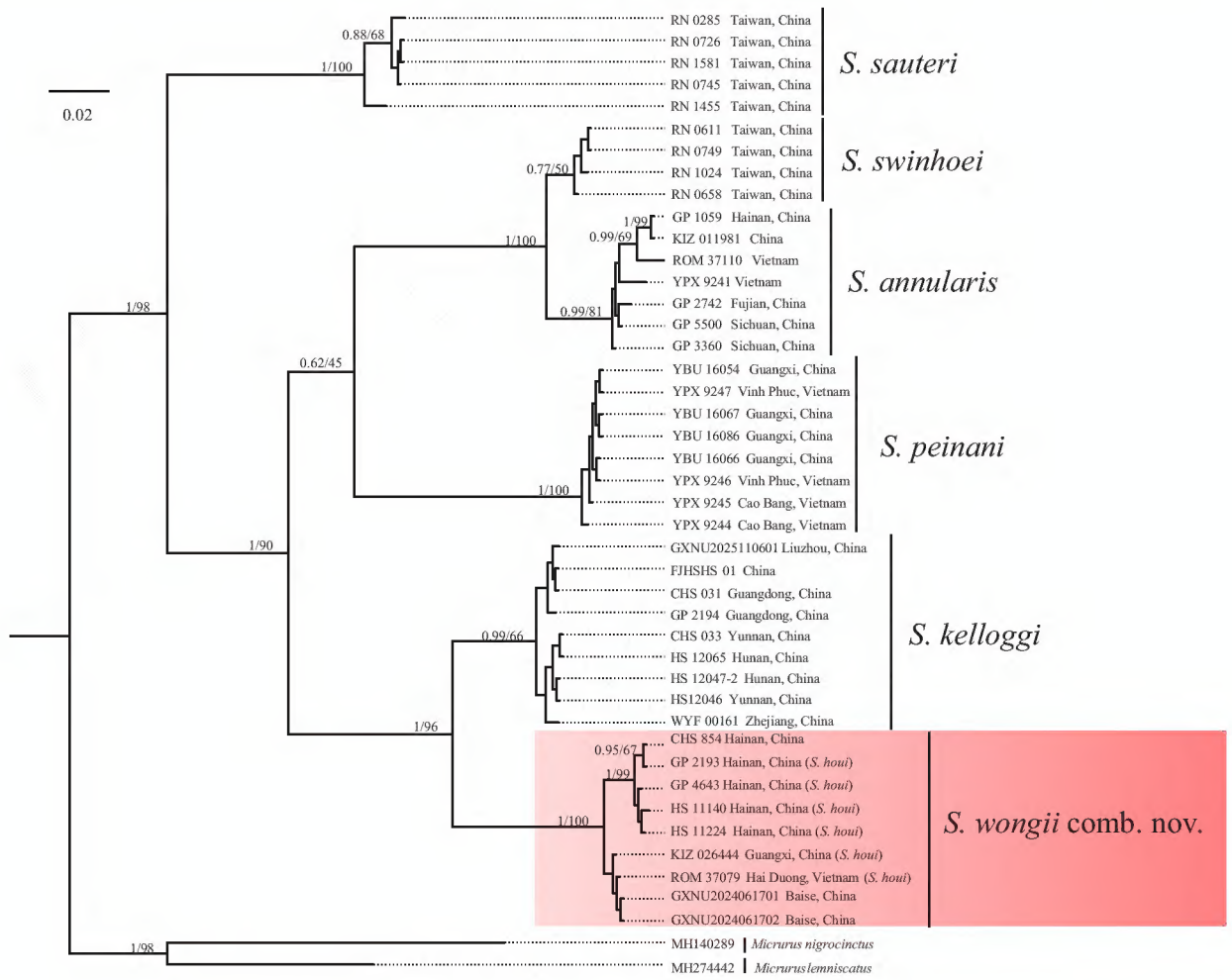

Figure 3. Phylogenetic relationships of *Sinomicrurus* species based on COI. Bayesian posterior probabilities (BPP) and standard bootstrap approximation (SBA) are denoted beside the major nodes.

Table 3. Uncorrected *p*-distances (in %) between *Sinomicrurus* species based on 630 base pairs from the mitochondrial gene COI.

No.	Taxa	1–2	3	4–8	9–16	17–23	24–27	28–35	36	37–42
1–2	*S. wongii* comb. nov.									
3	*S. kelloggi*	7.9								
4–8	*S. sauteri*	15.4–15.9	12.8–13.1	0.0–1.3						
9–16	*S. peinani*	14.9–15.1	13.8–14.1	16.8–17.4	0.0–0.2					
17–23	*S. annularis*	16.5–17.8	13.5–14.8	16.4–17.8	12.8–14.3	0.0–1.9				
24–27	*S. swinhoei*	15.8	13.3–13.8	14.9–15.7	12.8–13.5	3.0–4.4	0.0–0.4			
28–35	*S. kelloggi*	7.7–8.1	0.2–0.9	12.8–14.3	14.1–15.3	13.8–15.8	13.5–14.7	0.0–0.9		
36	*S. wongii* comb. nov.	1.3	9.0	15.7–16.2	14.6–14.9	17.3–18.6	15.8–16.5	8.8–9.2		
37–42	*S. wongii* comb. nov.	0.0–1.3	7.9–9.0	15.4–16.7	14.6–15.1	16.5–18.6	16.5	7.7–9.2	0.0–1.3	0.0–1.3

specimen (CHS 854) from Hainan is *S. wongii* comb. nov. rather than *S. kelloggi*, which is also corroborated by the uncorrected genetic distances based on the Cyt *b* gene. The uncorrected *p*-distance based on the Cyt *b* gene between the Napo specimens and the northern Vietnam specimens (ROM 37080 and ROM 35247) ranges 0.2–1.4%, and that between the Napo specimens and *S. kelloggi* ranges 5.5–6.1%, which is greater than the known interspecific *p*-distance of 4.5–5.1% between *S. annularis* and *S. swinhoei*.

Systematics

***Sinomicrurus wongii* (Fan, 1931), comb. nov.**

Suggest English name. Yaoshan coral snake.

Suggest Chinese name. 瑶山华珊瑚蛇 (Yáo Shān Huá Shān Hú Shé).

Synonyms. *Calliophis wongii* Fan, 1931.

Sinomicrurus houi Wang, Peng & Huang, 2018.

Sinomicrurus kelloggi Smart et al. (2021) (pro partim).

Description of GXNU2024061701. Adult male collected from Napo County, Baise City, Guangxi Zhuang Autonomous Region, China (23.3718°N, 105.7789°E, elevation 990 m a.s.l.) on 13 June 2024 by Li Ding and Wei Li. Total length 549 mm (SVL 493 mm, TaL 56 mm, TaL/ToL 10.2%); head distinctly distinct from the neck; prefrontal slightly longer than width, contacting the rostral, nasal, and frontal laterally; frontal subequally in length and width, contacting the prefrontal, nasal, preocular, supraocular, and parietal laterally; one preocular, in contact with the nasal; loreal absent; two postocular; one supraocular, approximately twice as long as wide; parietal shield-shaped; 1 + 2 temporals; the 3rd and 4th supralabial bordering the eye, sixth largest and longest; first pair infralabial in contact behind mental, second small, from first to third touching anterior chin-shields, 4th largest and contacting posterior chin-shield; 15–15–15 dorsal scale rows, dorsal scales smooth; anal

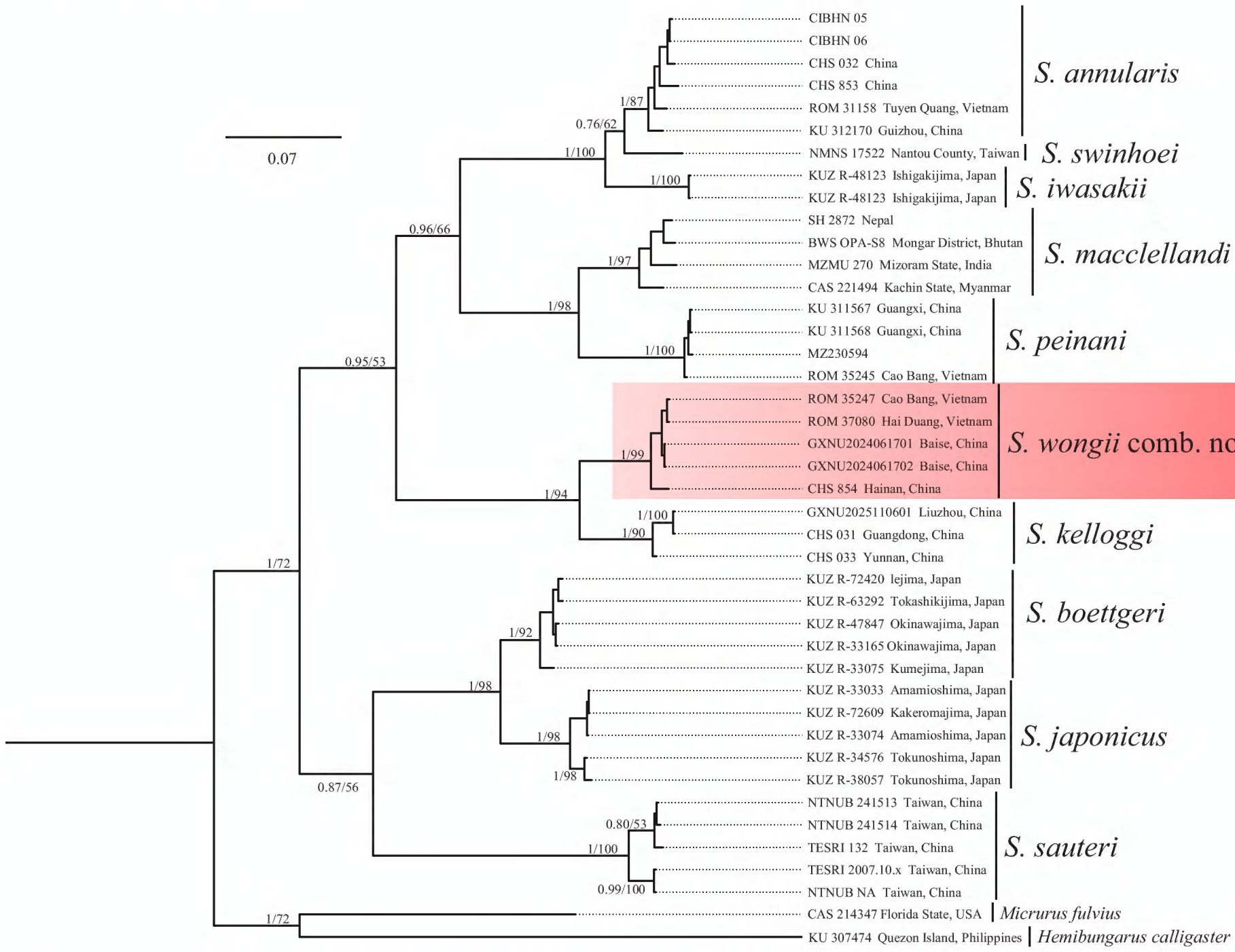

Figure 4. Phylogenetic relationships of *Sinomicrurus* species based on Cyt *b*. Bayesian posterior probabilities (BPP) and standard bootstrap approximation (SBA) are denoted beside the major nodes.

plate divided; 30 subcaudals, paired; tail complete, tip round. In life, dorsum of head black, with two transverse white bands: one narrow white broadwise band in the forefront of head, covering almost all the 3rd, 4th,5th supralabials, preoculars, and continuing through forefront prefrontals; the other much broader band at the posterior part appearing in a "V" shape (Fig. 5I), with its anterior margin located at the posterior supralabials, apex reaching the posterior end of the frontal, from both sides of frontal to neck sides and gradually widening; Ventral surface creamy yellow; dorsum of body rufous brown; black dorsal bands finely edged with pale pinkish buff; 19 regular dorsal bands on body (all crossing the midline), only half a scale wide; 3 dorsal bands on tail; 39 black blotches on ventral scales; 5 black blotches on subcaudal.

Description of GXNU2024061702. Adult female collected from Napo County, Baise City, Guangxi Zhuang Autonomous Region, China (23.3718°N, 105.7789°E, elevation 990 m a.s.l.) on 13 June 2024 by Li Ding and Wei Li. Tail length 63 mm; mid- and posterior dorsal scale rows 15, anterior dorsal scale rows unidentifiable; ventrals 187; subcaudals 34; anal plate divided; loreal absent; 1 preocular; 2 postoculars; 4 dorsal bands on tail; dorsum of head black, with two transverse white bands: one narrow white broadwise band in the forefront of head, the other much broader band at the posterior part appearing in a "V" shape (Fig. 5J); Ventral surface creamy yellow; dorsum of body rufous brown; dorsal bands on body only half a scale wide; other characters unidentifiable.

Variation. Tail length for adults 44–73 mm, total length 454–629 mm (n = 9). Coloration: *S. wongii* comb. nov. from Hainan Island is scarlet, whereas the continental populations are rufous brown. White bang on the dorsal head: The white bangs on the dorsal head of Hainan Island specimens are shaped like the Chinese character "八," while the continental specimens are "V"-shaped.

Comparison with *S. kelloggi*. The two species share the same number of dorsal scale rows, supralabials, preoculars and postoculars, with no obvious differences observed in other scalation characters or morphometric traits. *S. wongii* comb. nov. has 7 infralabials, whereas *S. kelloggi* has only 6. The black transverse bands on the dorsal body of *S. wongii* comb. nov. are merely half a scale wide, while those of *S. kelloggi* are one scale wide (Fig. 1). Specimen (MLP1404033R) reported by Sun et al. (2015) from Laojunshan, Yunnan, has 15 dorsal scale rows and 7 infralabials, and the trunk black transverse bands are only a half scale wide. Based on the data of the present study, it

Table 4. Uncorrected *p*-distances (in %) between *Sinomicrurus* species based on 1050 base pairs from the mitochondrial gene Cyt *b*.

No.	Taxa	1–2	3	4–9	10–14	15–16	17–21	22–24	25–26	27–30	31–34	35–39
1–2	*S. wongii* comb. nov.											
3	*S. kelloggi*	6.1										
4–9	*S. annularis*	20.0–21.6	18.2–20.0	0.6–2.0								
10–14	*S. boettgeri*	16.8–17.3	17.6–18.1	17.9–21.3	0.0–1.8							
15–16	*S. iwasakii*	19.0	19.1	6.8–7.9	20.4–21.2	0.0						
17–21	*S. japonicus*	20.2	18.9	20.8–22.4	7.6–8.9	20.8–21.5	0.0–2.4					
22–24	*S. wongii* comb. nov.	0.2–1.4	6.3–6.8	20.3–21.9	17.1–17.6	19.3	19.9–22.0	0.0–1.6				
25–26	*S. kelloggi*	5.5–6.1	0.0–1.2	18.2–20.0	17.1–18.1	19.0–19.1	18.8–18.9	5.7–6.8	1.2			
27–30	*S. macclellandi*	14.4–15.5	16.5–17.6	15.8–18.3	19.7–21.1	16.6–17.1	23.5–24.6	14.0–15.7	16.5–17.9	0.8–2.8		
31–34	*S. peinani*	16.2–16.7	19.4–20.0	15.7–18.1	20.7–22.1	17.5–18.1	24.3–25.0	16.2–17.6	19.2–20.0	7.7–8.6	0.0–0.4	
35–39	*S. sauteri*	19.2–21.0	17.7–19.5	19.5–20.7	16.8–18.9	22.5–23.5	19.1–20.4	18.9–22.1	17.7–19.7	21.7–23.8	22.9–23.6	0.0–2.4
40	*S. swinhoei*	19.5	19.3	4.5–5.1	17.9–18.8	7.7	19.1–19.4	19.8–20.6	18.7–19.3	17.4–18.5	17.3–17.8	20.4–20.8

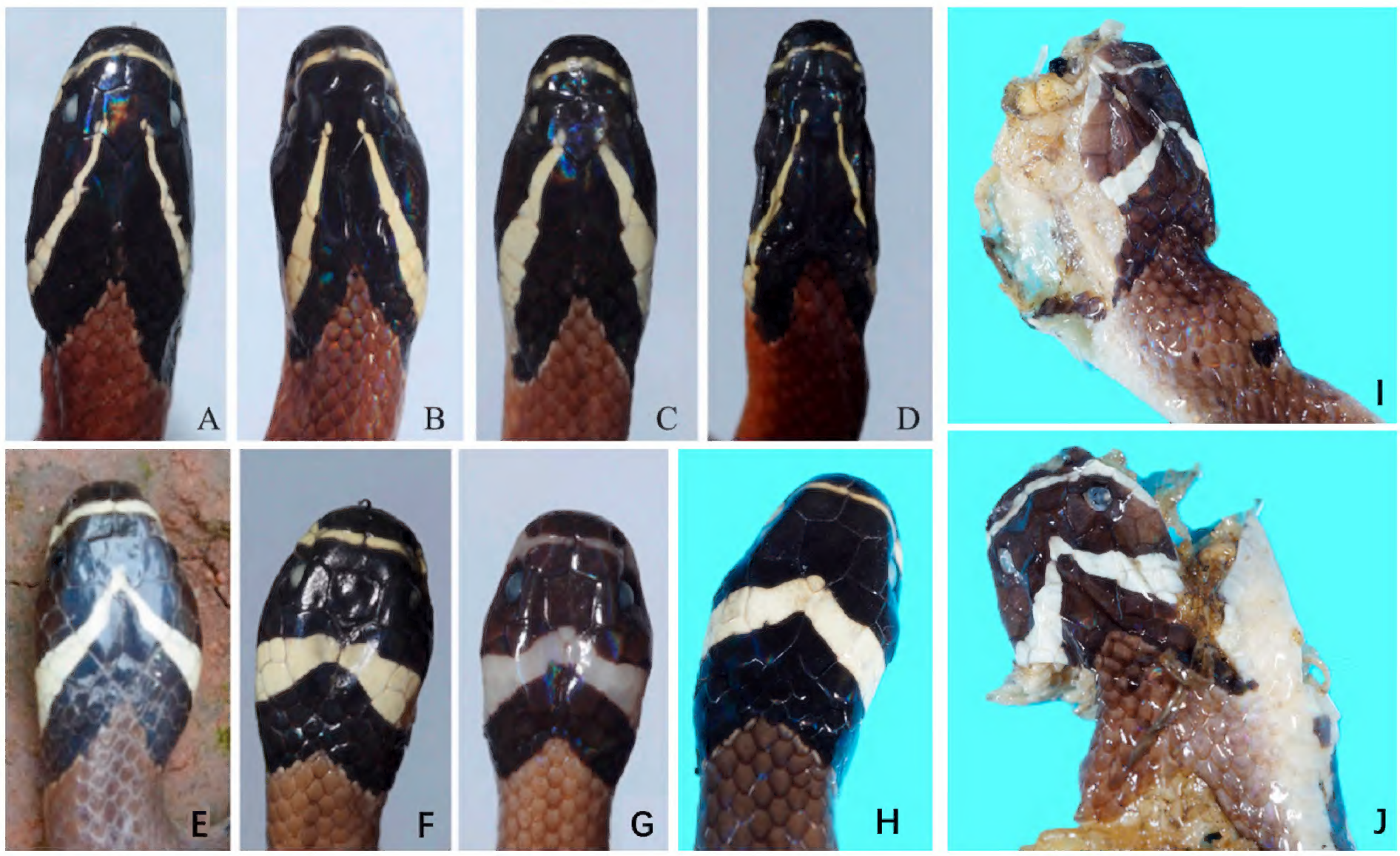

Figure 5. Dorsal views of the head of *S. wongii* comb. nov. and *S. kelloggi*: **A–D.** *S. wongii* comb. nov. from Hainan (Peng et al. 2018); **E.** *S. wongii* comb. nov. from Yunnan (Sun et al. 2015); **F, G.** *S. kelloggi* from Yunnan Province (Wang et al. 2015) and Anhui (Chen et al. 2013); **H.** *S. kelloggi* (GXNU2025110601) from Rongshui, Liuzhou, Guangxi; **I, J.** *S. wongii* comb. nov. (GXNU2024061701, GXNU2024061702) from Napo, Baise, Guangxi. For *S. kelloggi*, the broad white stripe on the dorsal head is "V"-shaped, with the stripe converging at the midline of the head. For *S. wongii* comb. nov. from Hainan Island, the broad white stripe on the dorsal head resembles the Chinese character "⺆." In contrast, *S. wongii* comb. nov. from the mainland has a "V"-shaped stripe.

should be referred to as *S. wongii* comb. nov. rather than *S. kelloggi*.

Diagnosis. This species is characterized by the following combination of characters: (1) dorsal scale rows 15–15–15, smooth throughout; (2) no loreal; (3) 1 preocular,

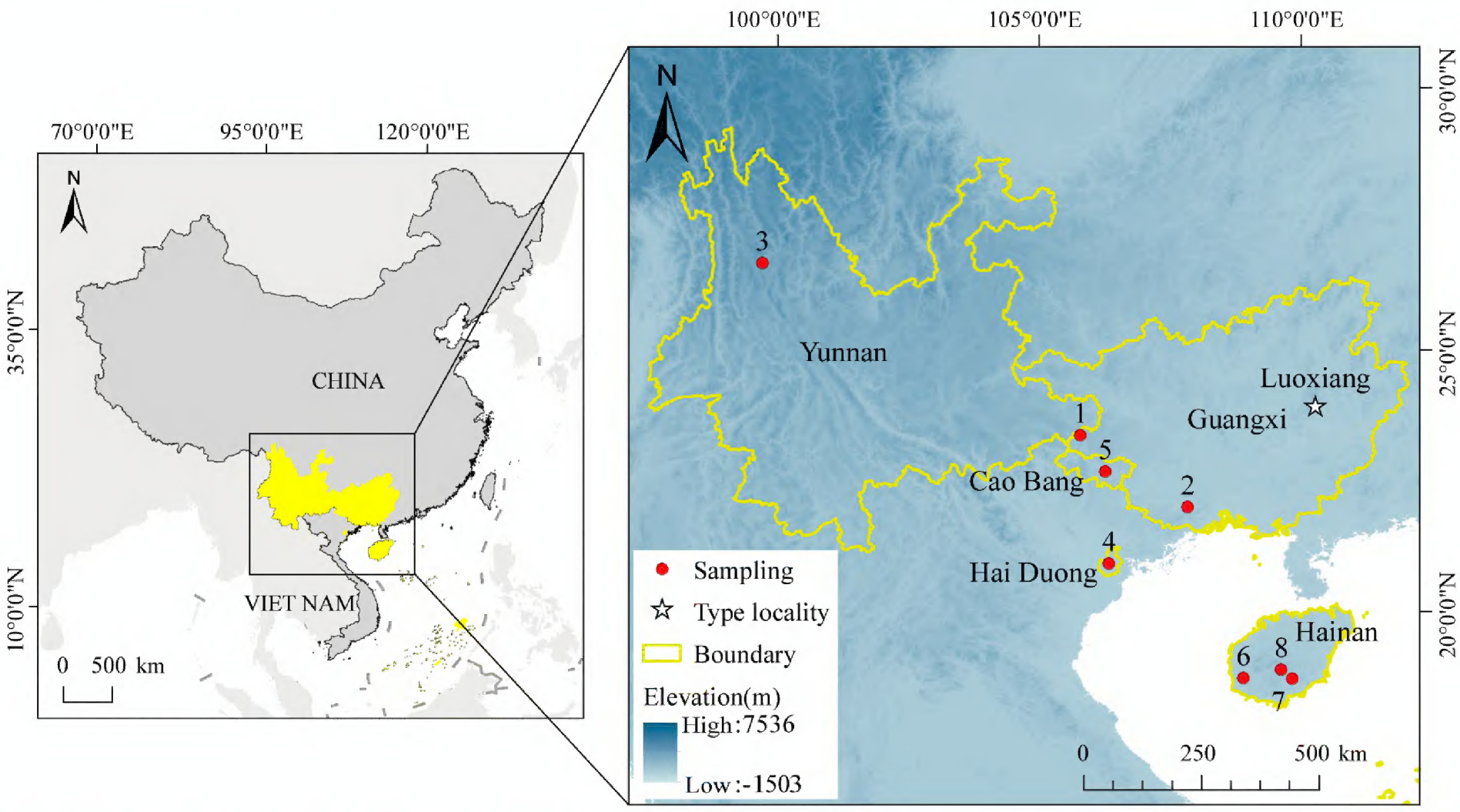

Figure 6. Distribution map of *S. wongii* comb. nov. Star indicates the type locality: Luoxiang Township, Jinxiu Yao Autonomous County, Laibin City. Red dots represent the currently known distribution localities. Information for each locality is as follows: **1.** Napo County, Baise City, Guangxi, which is the distribution discovered in this study; **2.** Shangsi County, Fangchenggang City, Guangxi; **3.** Laojun Mountain, Yunnan; **4.** Hai Duong Province; **5.** Cao Bang Province; **6.** Jianfengling, Hainan; **7.** Diaoluoshan, Hainan; **8.** Wuzhishan, Hainan.

2 postoculars; (4) 7 supralabials, 7 infralabials; (5) black dorsal bands finely edged with pale pinkish buff, each band only half a scale wide; (6) white markings on the dorsal surface of the head shaped like the Chinese character "丿\" or a "V" shape, with the opening angle of the "V" relatively small, forming an acute angle; (7) venter with 29–39 black blotches.

Distribution and ecology. *S. wongii* comb. nov. is so far known from Hainan, Guangxi and Yunnan of China, and Hai Duong and Cao Bang of Vietnam (Fig. 6). The adjacent habitat of the two *Sinomicrurus* specimens collected from Napo is composed of secondary evergreen broad-leaved forests interspersed with shrubs and vines (Fig. 7). Within this region, the species is sympatric with *Ptyas major* (Gunther, 1858), *Pareas formosensis* (Van Denburgh, 1909), *Ahaetulla prasina* (Boie, 1827), *Protobothrops mucrosquamatus* (Cantor, 1839), and *Trimeresurus albolabris* Gray, 1842.

Discussion

Integrating morphological and molecular evidence, this study reinstates *Calliophis wongii*'s status as an independent species, synonymizes *S. houi* with *C. wongii*, and reallocates the latter to the genus *Sinomicrurus* under the designation *Sinomicrurus wongii* comb. nov. This designation adheres to the priority principle of zoological nomenclature, as *C. wongii* was published earlier than *S. houi*.

Figure 7. Habitat of *S. wongii* (GXNU2024061701, GXNU2024061702), Napo County, Baise City, Guangxi Zhuang Autonomous Region, China.

For the Guangxi sample (GP4839), we observed unstable topological placement during phylogenetic tree

reconstruction, a problem consistent with that reported by Smart et al. (2021). Thus, we concur with their conclusion that the sequence of this sample may be problematic. Our phylogenetic analyses confirm that *S. wongii* comb. nov. is distributed in northern Vietnam, as the Vietnamese specimens (ROM 37079, ROM 37080, and ROM 35247) cluster with *S. wongii* comb. nov. specimens in the phylogenetic tree. Furthermore, uncorrected *p*-distance analysis reveals that their genetic distance from *S. wongii* comb. nov. is 0.0–1.4%, falling within the intraspecific range. Thus, these specimens are identified as *S. wongii* comb. nov.

For *C. wongii tonkinensis* Bourret, 1935, previously recognized as a subspecies of *Calliophis wongii*, future sampling should be conducted at its type locality to confirm whether it represents an independent lineage or a subspecies.

Acknowledgments

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References

Bourret RL (1935) Notes herpétologiques sur l'Indochine française. X. Les Serpents de la station d'altitude du Tam- dao. Bulletin Générale de l'instruction Publique, Hanoi 15(8): 259–271.

Che J, Chen HM, Yang JX, Jin JQ, Jiang K, Yuan ZY, Murphy RW, Zhang YP (2012) Universal COI primers for DNA barcoding amphibians. Molecular Ecology Resource 12(2): 247–258. https://doi.org/10.1111/j.1755-0998.2011.03090.x

Chen JM, Tang XS, Huang S (2013) *Sinomicrurus kelloggi* Firstly Found in Anhui Province, China. Chinese Journal of Zoology 48(1): 134–135. [In Chinese]

Fan TH (1931) Preliminary report of reptiles from Yaoshan, Kwangsi, China. Kuo-li chung-shan ta-hsüeh. Sheng-wu-hsueh-his, iv+154pp. [pls 1–5]

Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Molecular Biology and Evolution 35(6): 1547–1549. https://doi.org/10.1093/molbev/msy096

Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B (2017) PartitionFinder 2: New methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Molecular Biology and Evolution 34(3): 772–773. https://doi.org/10.1093/molbev/msw260

Liu Q, Yan JW, Hou SB, Wang P, Nguyen SN, Murphy RW, Che J, Guo P (2020) A new species of the genus *Sinomicrurus* (Serpentes: Elapidae) from China and Vietnam. Zoological Research 41(2): 194–198. https://doi.org/10.24272/j.issn.2095-8137.2020.023

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32(1): 268–274. https://doi.org/10.1093/molbev/msu300

Peng LF, Wang LJ, Ding L, Zhu YW, Luo J, Yang DC, Huang RY, Lv SQ, Huang S (2018) A new species of the genus *Sinomicrurus* Slowinski, Boundy & Lawson, 2001(Squamata: Elapidae) from Hainan Province, China. Asian Herpetological Research 9(2): 65–73. https://doi.org/10.16373/j.cnki.ahr.170090

Pope CH (1928) Seven new reptiles from Fukien Province, China. American Museum Novitates 320: 1–6.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Slowinski JB, Boundy J, Lawson R (2001) The phylogenetic relationships of Asian coral snakes (Elapidae: Calliophis and Maticora) based on morphological and molecular characters. Herpetologica 57(2): 233–245.

Smart U, Ingrasci MJ, Sarker GC, Lalremsanga H, Murphy RW, Ota H, Tu MC, Shouche Y, Orlov NL, Smith EN (2021) A comprehensive appraisal of evolutionary diversity in venomous Asian coralsnakes of the genus *Sinomicrurus* (Serpentes: Elapidae) using Bayesian coalescent inference and supervised machine learning. Journal of Zoological Systematics and Evolutionary Research 59(8): 2212–2277. https://doi.org/10.1111/jzs.12547

Smith EN, Campbell JA (1994) A new species of *Rhadinaea* (Colubridae) from the Caribbean versant of Guatemala. Occasional Papers of the Museum of Natural History of the University of Kansas 167: 1–9.

Smith EN, Arachchi KM, Somaweera R (2008) A new species of coralsnake of the genus *Calliophis* (Squamata: Elapidae) from the Central Province of Sri Lanka. Zootaxa 1847(1): 19–33. https://doi.org/10.5281/zenodo.183338

Sun GZ, Luo WX, Wang JS (2015) *Sinomicrurus kelloggi* Found in Laojunshan, Yunnan, China. Chinese Journal of Zoology 50(2): 242. [In Chinese] http://dx.doi.org/DOI:10.13859/j.cjz.201502022

Uetz P, Freed P, Aguilar R, Reyes F, Kudera J, Hošek J [Eds] (2026) The Reptile Database. https://reptile-database.reptarium.cz/ [Accessed January 2026] https://doi.org/10.48580/d37s.v31

Vogel G, David P (2010) A new species of the genus *Lycodon* (Boie, 1826) from Yunnan Province, China (Serpentes: Colubridae). Bonn Zoological Bulletin 57(2): 289–296. https://doi.org/10.5281/zenodo.15915238

Vogel G, Luo J (2011) A new species of the genus *Lycodon* (Boie, 1826) from the southwestern mountains of China (Squamata: Colubridae). Zootaxa 2807(1): 29–40. https://doi.org/10.11646/zootaxa.2807.1.2

Wang DQ, Yang DC, Peng LF, Cheng ZW, Xu JC, Hu XQ, Huang S (2015) *Sinomicrurus kelloggi* Firstly Found in Yunnan Province, China. Sichuan Journal of Zoology 34(2): 314. [In Chinese]

Zhang D, Gao F, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20(1): 348–355. https://doi.org/10.1111/1755-0998.13096

Appendix 1

Table A1. Morphometric and meristic data of the three collected specimens.

Characters/No./Sex	GXNU2025110601 Female	GXNU2024061701 Male	GXNU2024061702 Female	No. 1039 Male	No. 2041 Male	MLP1404033R NA	HUM20170001 Male	Re5410 Male	CIB108251 Female	HUM20170004 Female	*S. wongii* comb. nov. n = 9, Range	*S. kelloggi* n = 13, Range
Snout-vent length	523	493	–	410	443	545	556	476	500	499	410–556	412–557
Tail length	66	56	63	44	48	72	73	60	57	71	44–73	43–73
Total length	589	549	–	454	491	617	629	536	557	570	454–629	473–630
Tail length/total length	0.1121	0.1020	–	0.0969	0.0976	0.1167	0.1172	0.1119	0.1023	0.1161	0.0969–0.1172	0.0801–0.1309
Head length	16.0	–	–	–	–	10.9	22.0	21.2	18.2	22.0	18.2–22.0	13.0–16.0
Head width	9.7	–	–	–	–	10.8	10.9	10.2	9.0	10.5	9.0–10.9	9.0–11.0
Head height	6.7	–	–	–	–	6.1	7.4	7.2	6.3	7.3	6.3–7.4	5.0–7.0
Head length/width	1.66	–	–	–	–	–	2.02	2.08	2.02	2.10	2.02–2.10	1.35–1.66
Perimeter at neck	24.3	–	–	–	–	–	34.0	29.0	25.6	23.0	23.0–34.0	22.0–29.0
Perimeter at midbody	36.6	–	–	–	–	–	45.0	36.0	32.0	32.0	32.0–45.0	24.0–36.58
Perimeter before vent	25.7	–	–	–	–	–	28.0	24.5	24.1	24.0	24.0–28.0	20.0–25.67
Perimeter at midbody/total length	0.0621	–	–	–	–	–	0.0715	0.0672	0.0575	0.0561	0.0561–0.0715	0.0447–0.0634
Eye lengthwise	2.0	–	–	–	–	–	2.2	3.2	2.0	2.1	2.0–3.2	1.8–2.5
Eye widthwise	1.7	–	–	–	–	–	2.2	3.2	2.0	2.1	2.0–3.2	2.0–2.2
Rostral width	3.9	–	–	–	–	–	4.0	3.8	3.5	3.2	3.2–4.0	3.5–4.5
Dorsal scale rows	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15-15	15-15–15
Ventrals	186	–	187	192	194	191	173	175	178	183	173–194	177–197
Subcaudals	32	30	34	29	30	33	35	28	32	34	28–35	27–36
Anal plate	divided	divided	divided	divided	divided	divided	divided	divided	divided	divided	divided	divided
Preoculars	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1
Postoculars	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2
Temporals	1+2	1+2	–	1+2	1+2	1+2/3	1+2	1+2	1+2	1+2	1+2	1+2
Supralabials	7/7	–	–	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7
Infralabials	6/6	–	–	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	6/6
Number of dorsal bands on body	20	19	–	19	20	21	16	16	19	18	16–21	19–24
Number of dorsal bands on tail	4	3	4	4	4	4	4	2	3	3	2–4	3–5
Number of blotches on ventral	41+7	39+5	–	–	–	39+7	34+7	29+5	36+6	36+6	29–39 + 5–7	37–48 + 5–9

Note: "–" indicates missing data.